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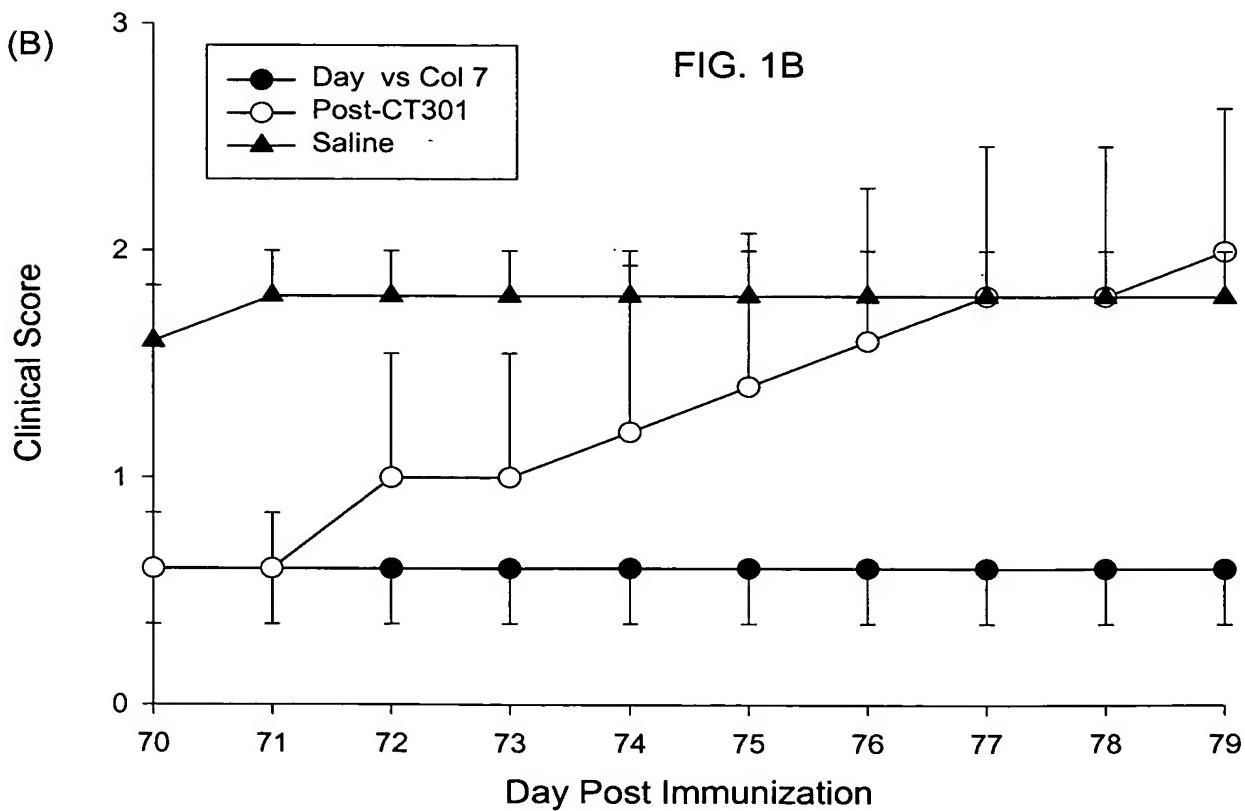
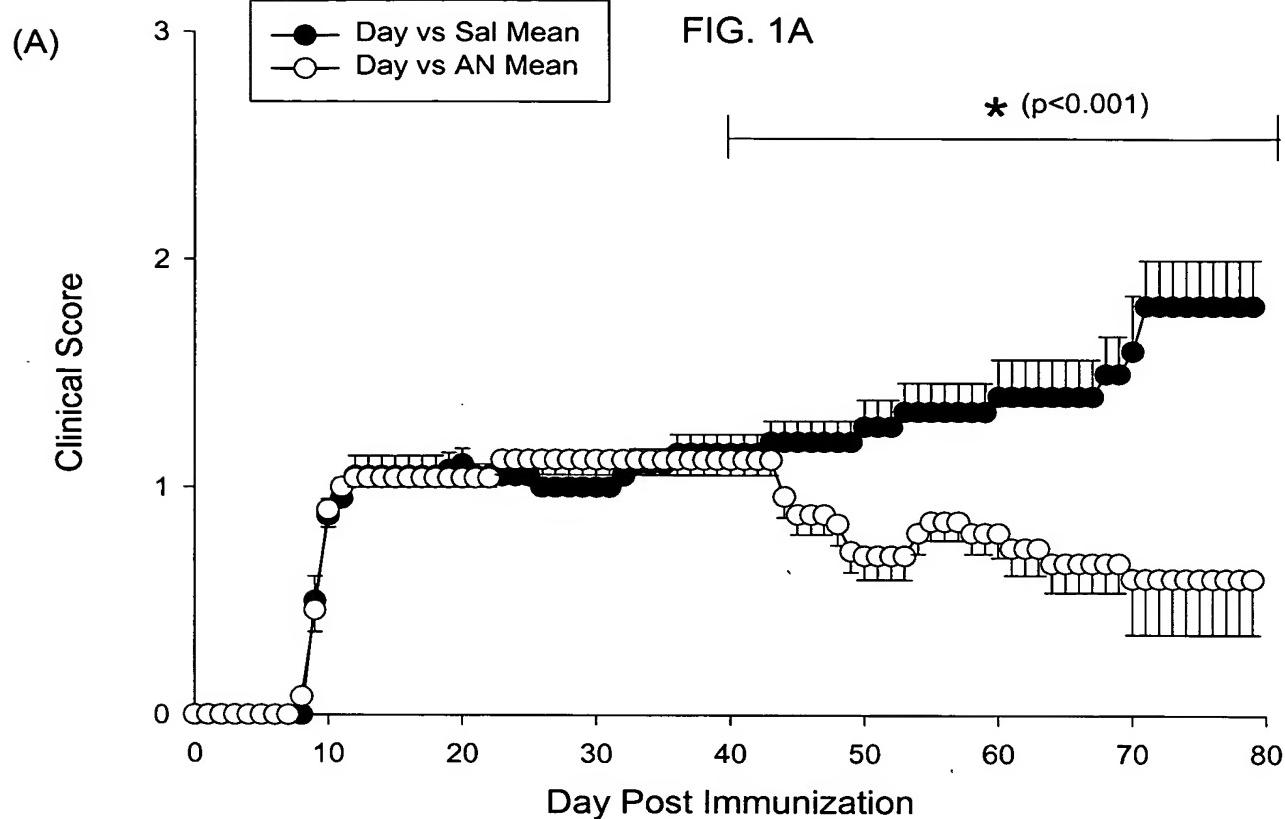




FIG. 2A

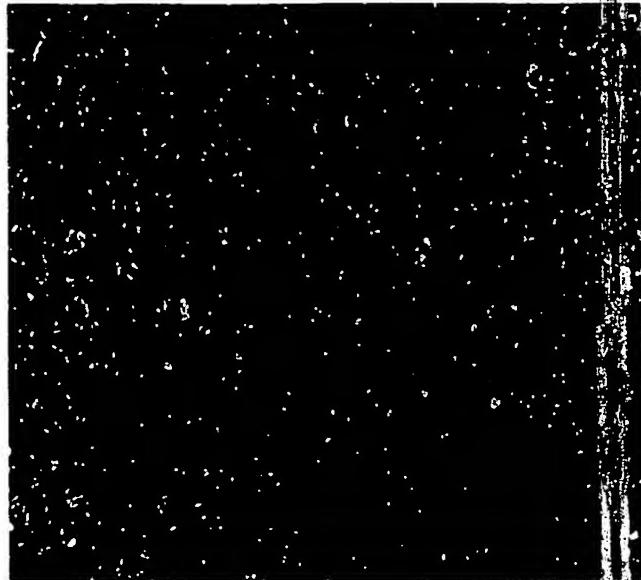


FIG. 2B



FIG. 2C

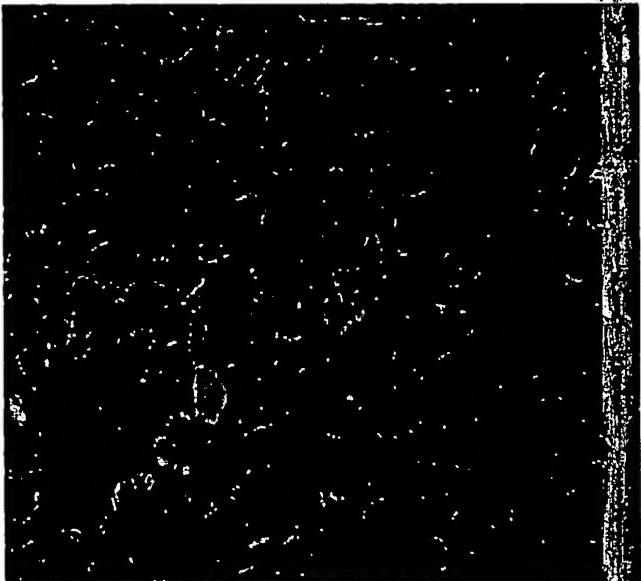


FIG. 2D

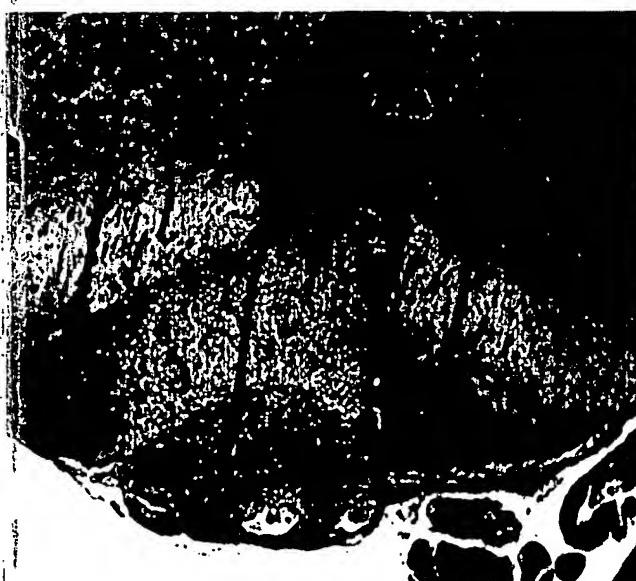


FIG. 2E

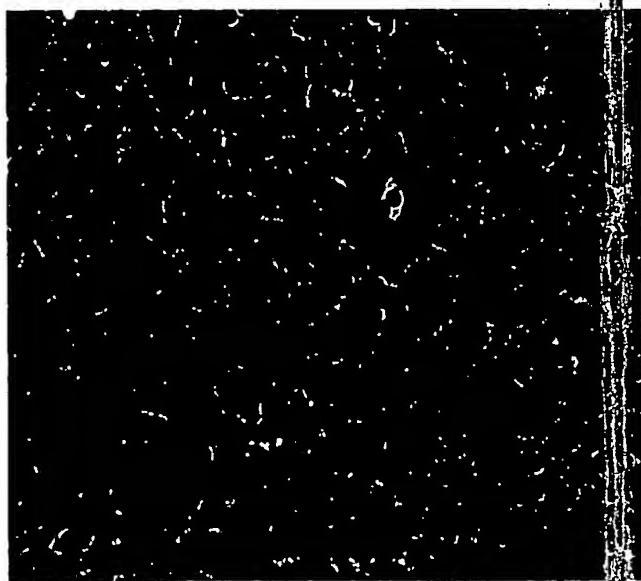


FIG. 2F



FIG. 2G



FIG. 2H

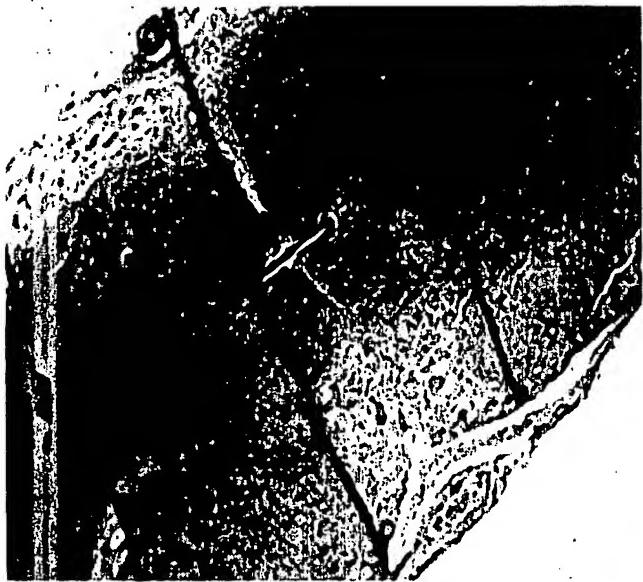


FIG. 2I

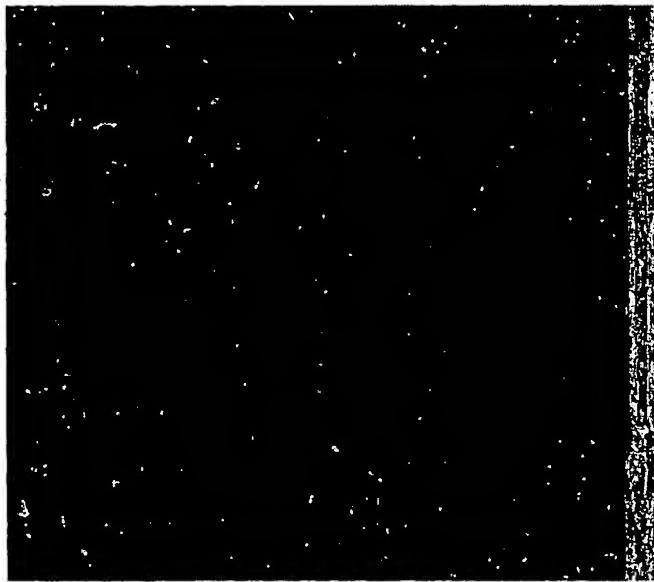


FIG. 2J

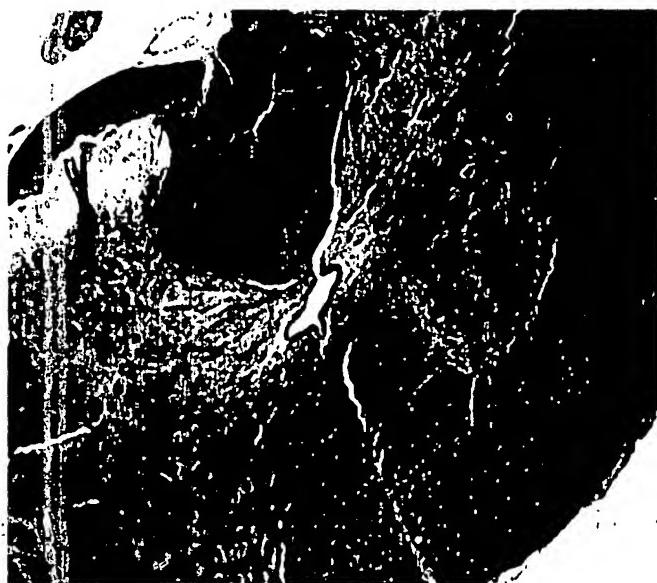
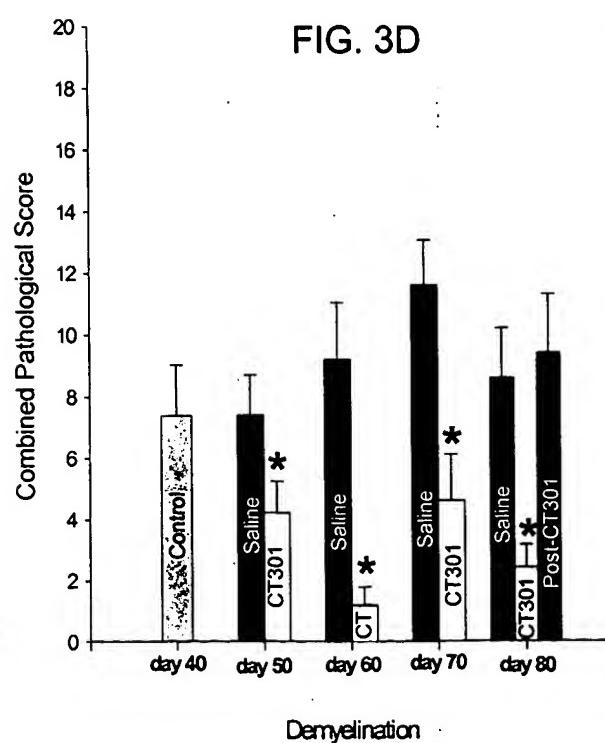
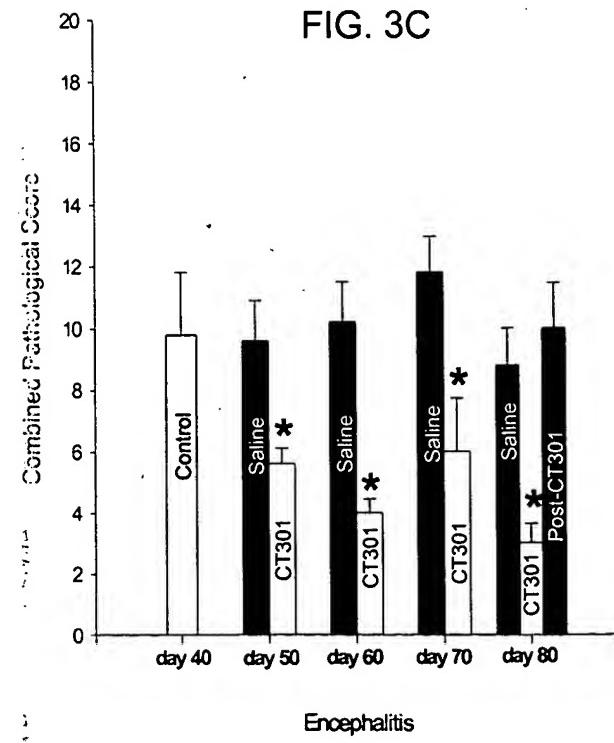
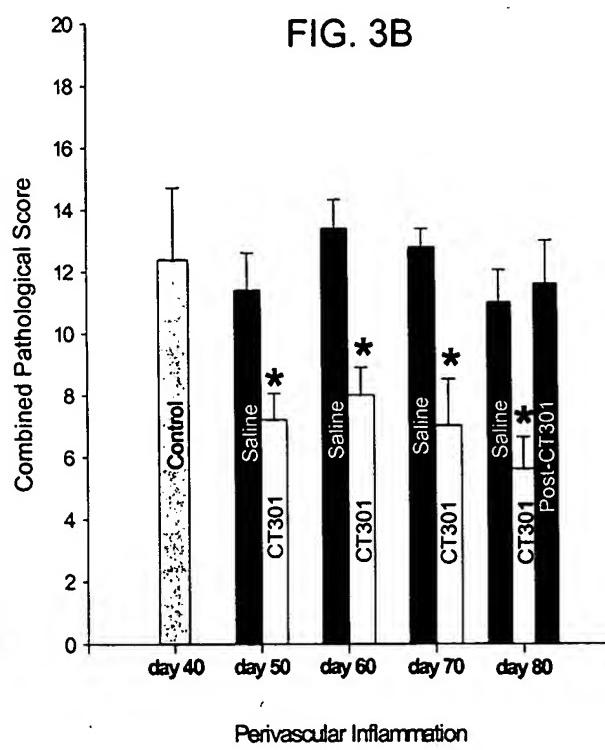
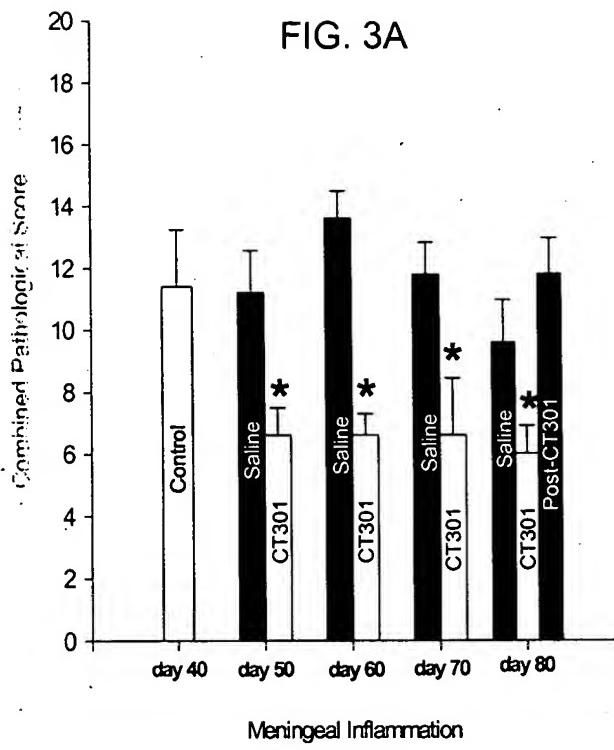


FIG. 2K



FIG. 2L



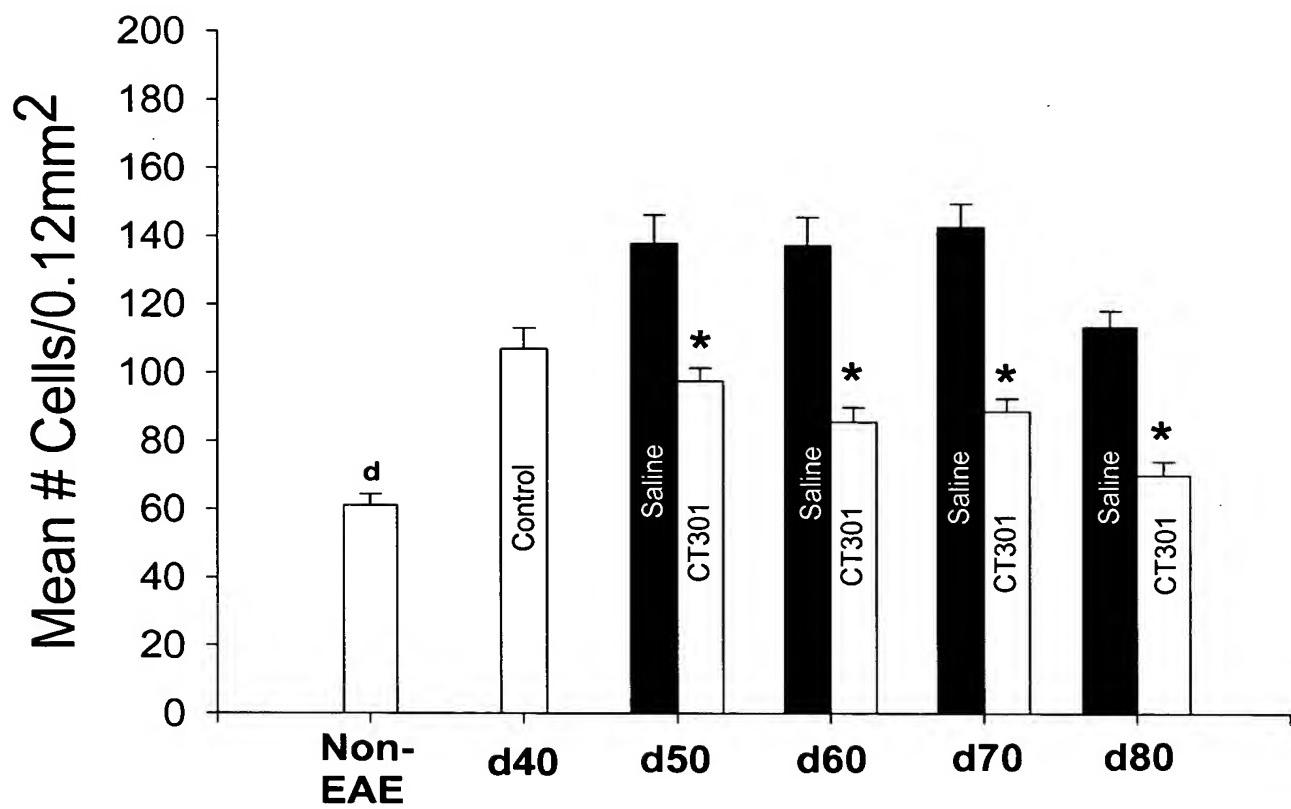
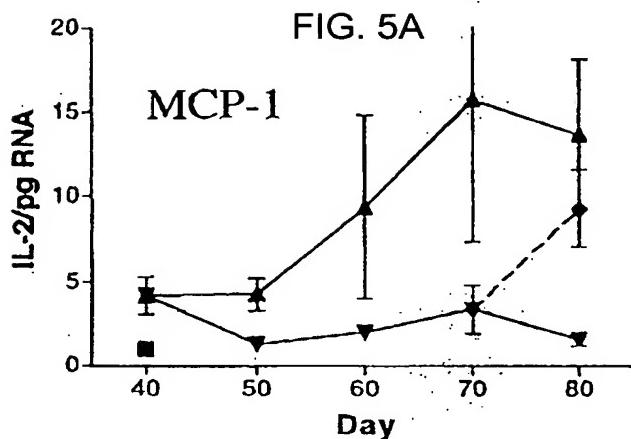
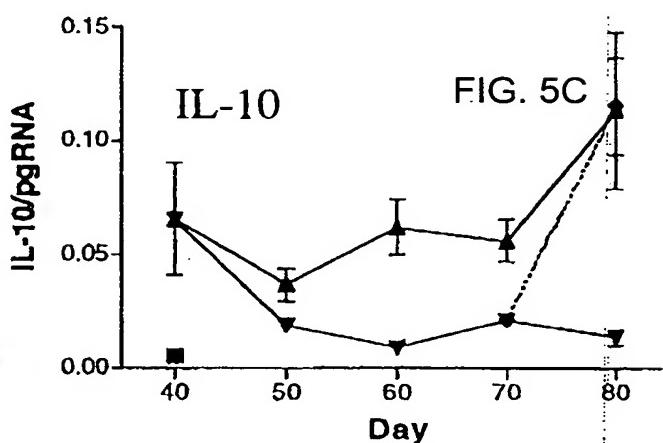
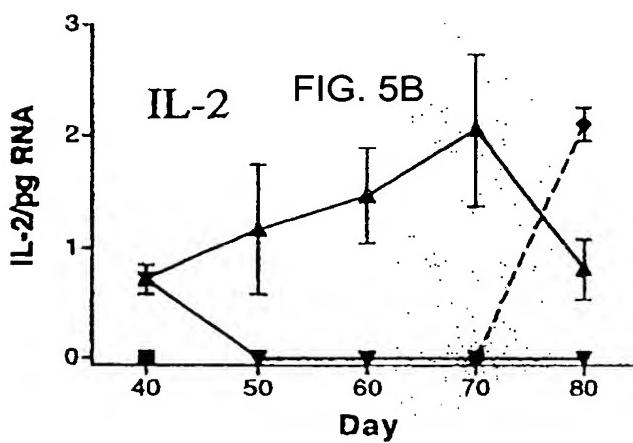


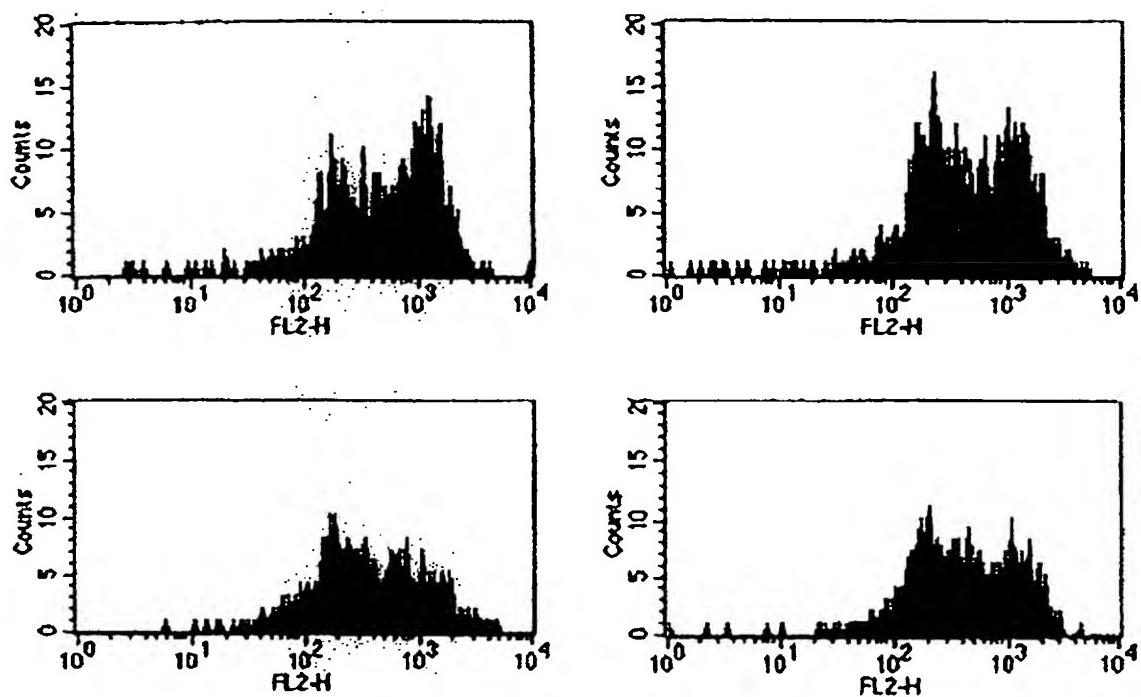
FIG. 4



■ Non EAE
▲ Saline Control
▼ CT301
··◆·· Post CT301



CT301



Saline

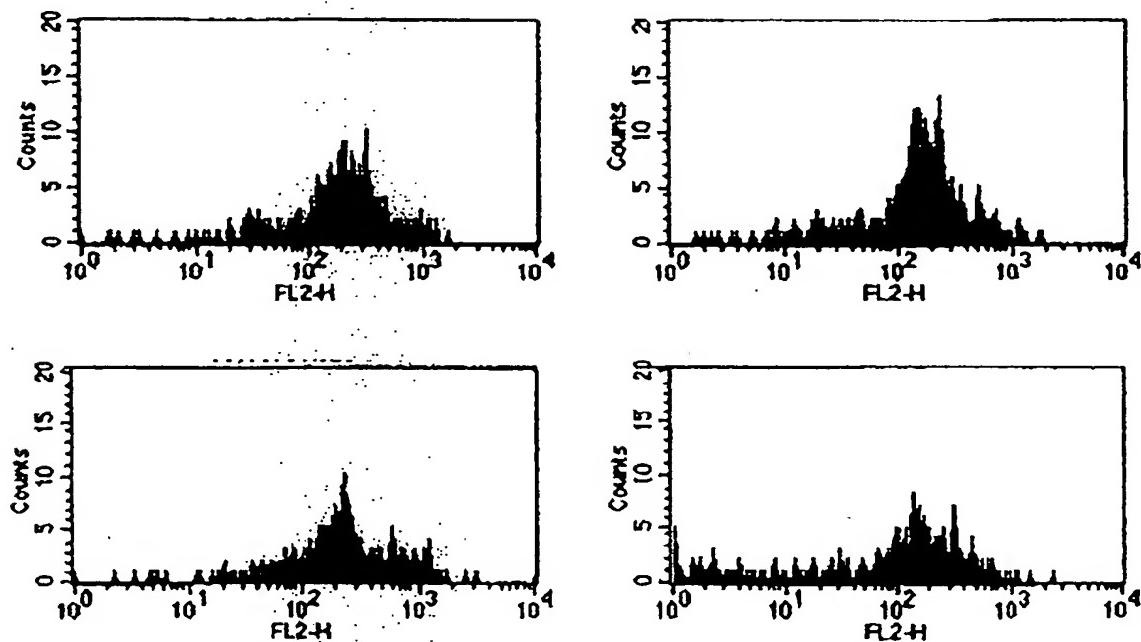


FIG. 6

Percentage α 4 Integrin-High Blood Lymphocytes

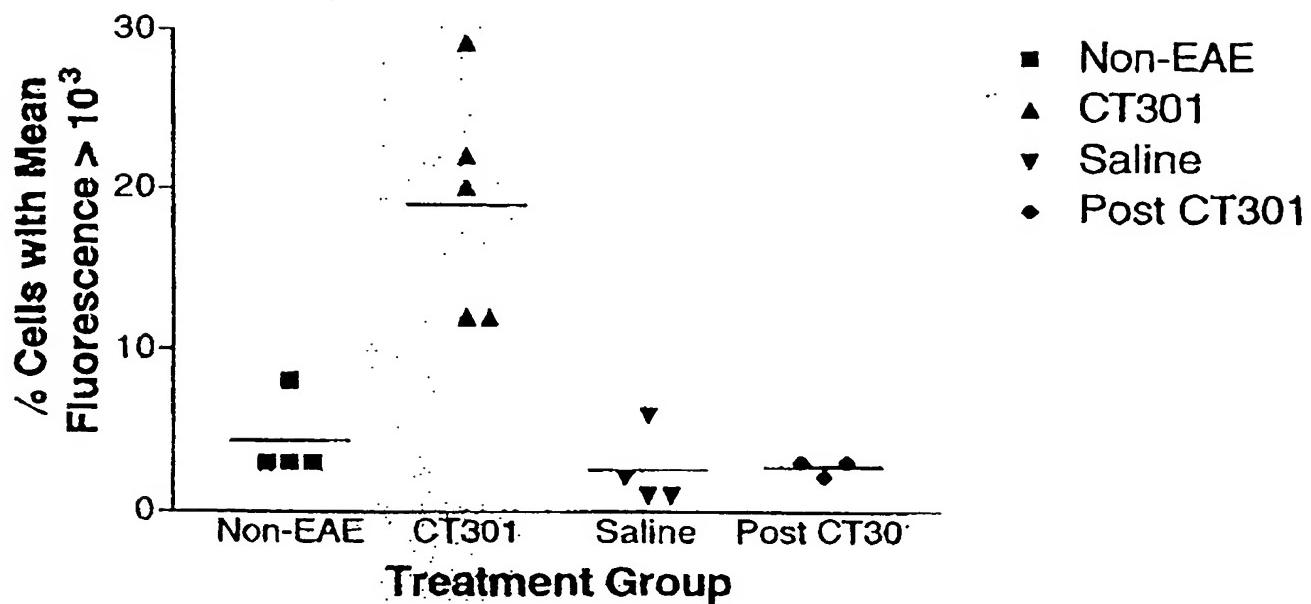


FIG. 7A

Expression of α 4 Integrin on Blood Monocytes

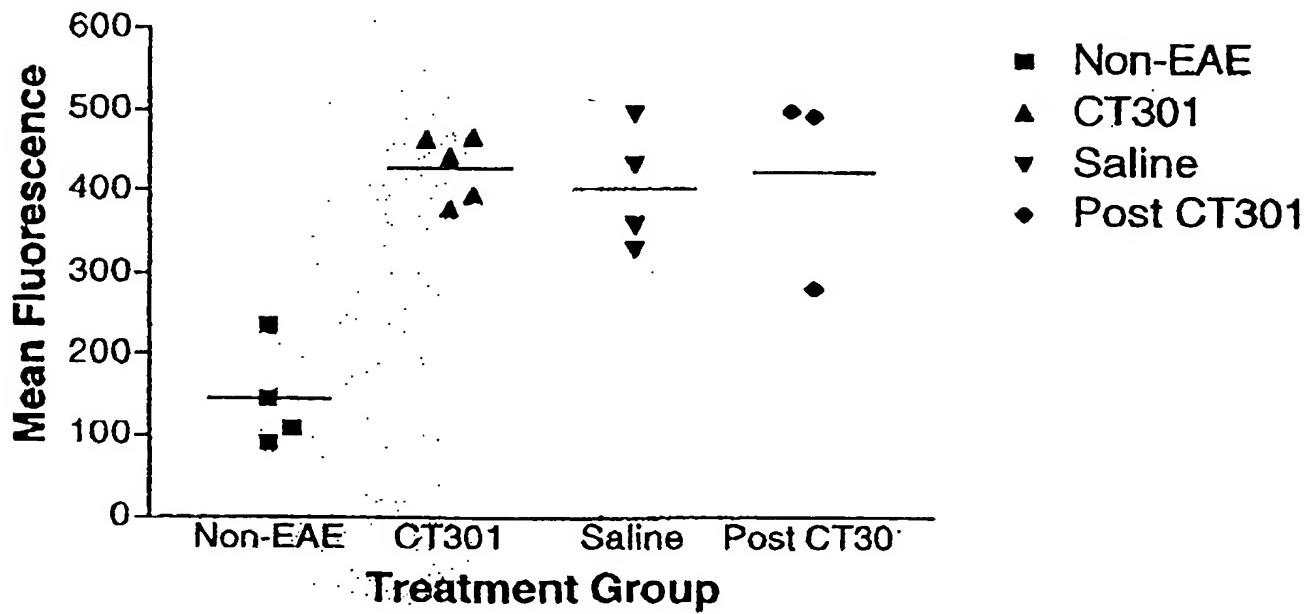
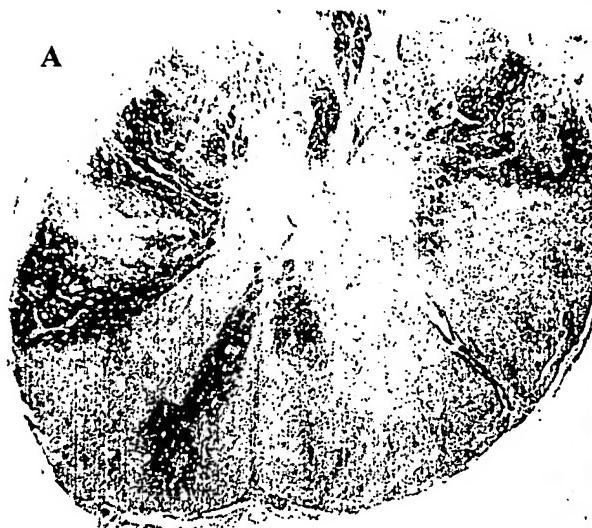
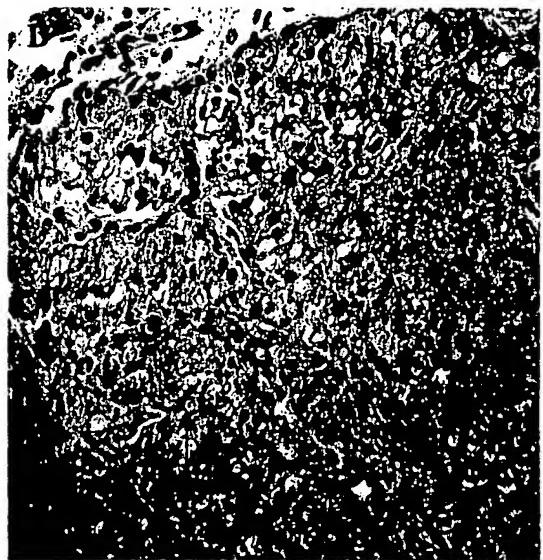
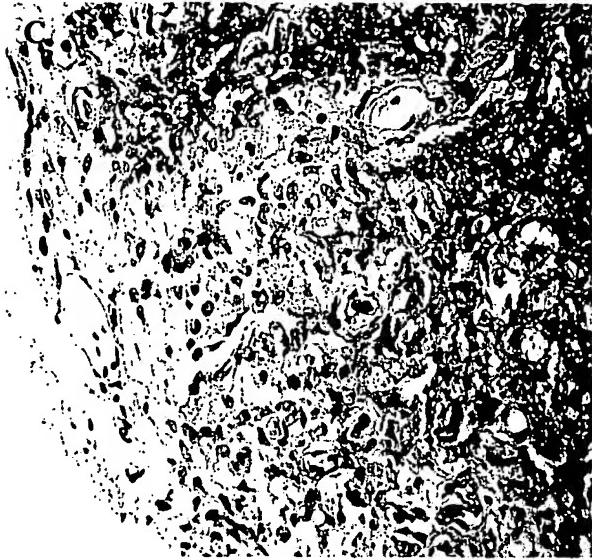


FIG. 7B

A



C



E

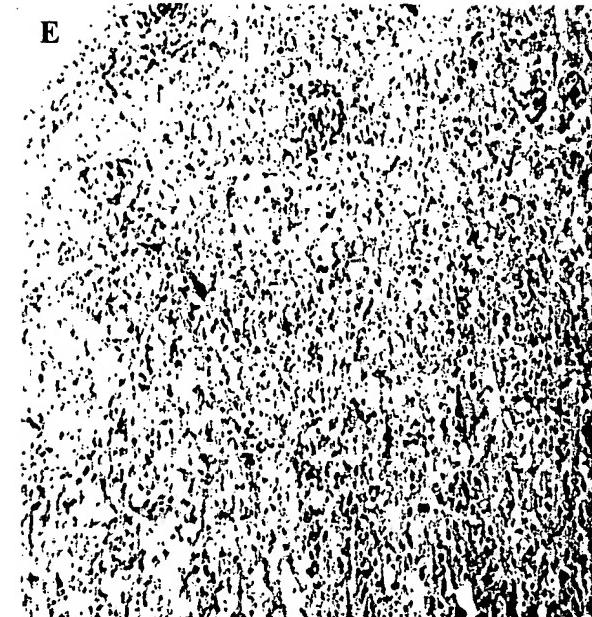


FIG. 8

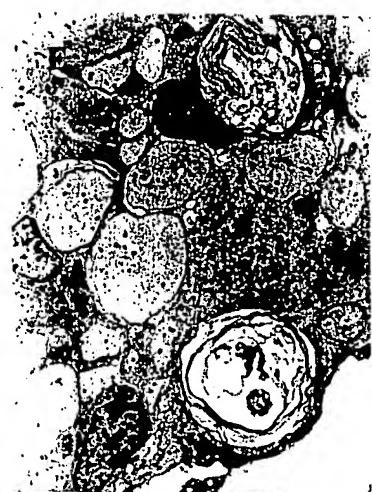
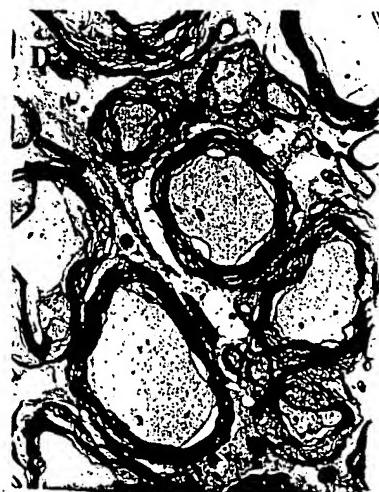
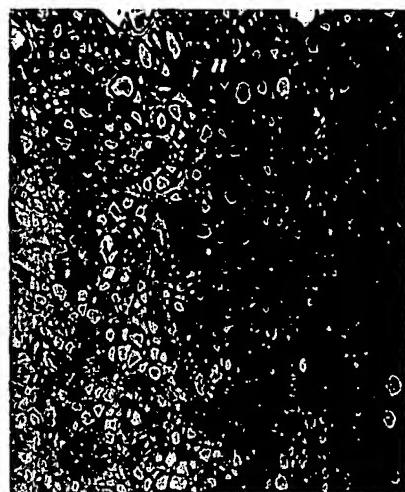
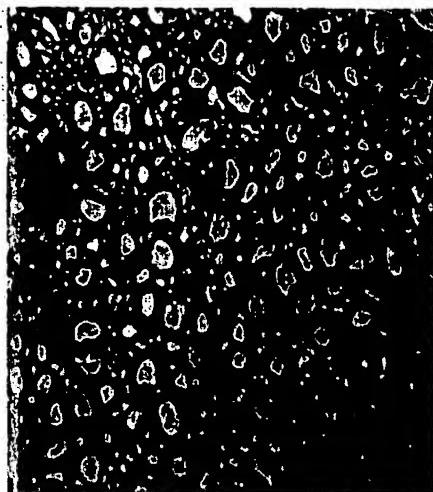


FIG. 9

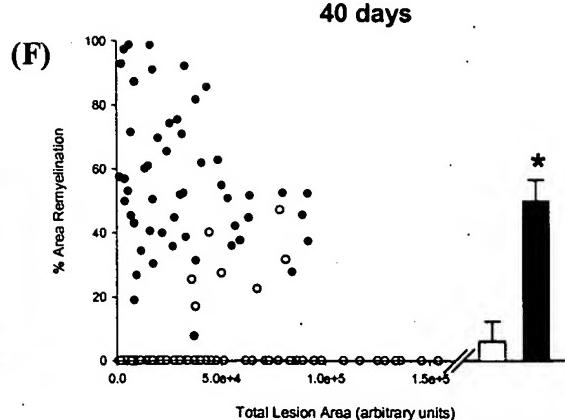
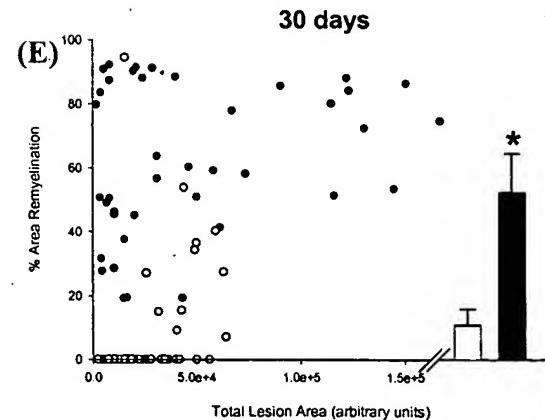
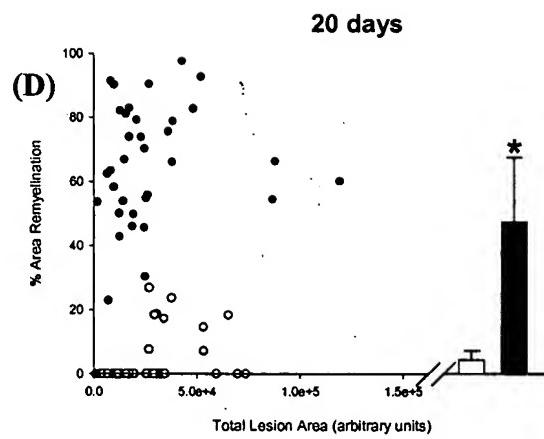
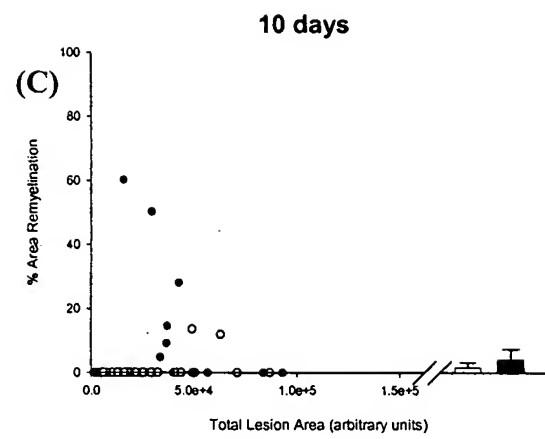
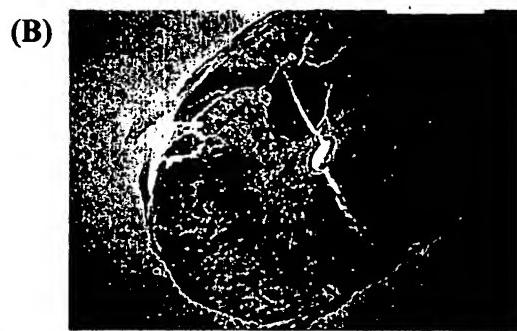
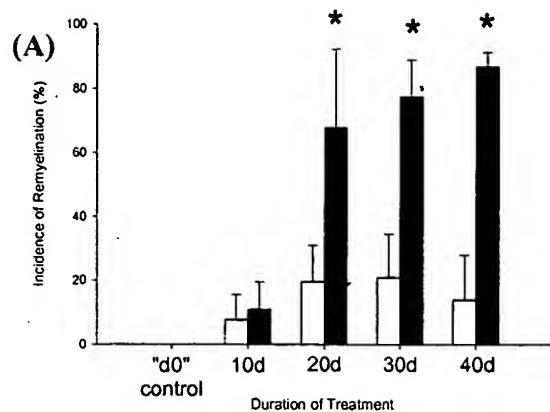


FIG. 10

1 atgaggggccccctgctcagattttggattcttggtcaggagacgttgt
1-----
tactcccggggacgagtcataaaaacctaagaaccaggctctgcaaca

49 agaaatgagaccgtctattcagttccctggggctttgttctggcttcatgg
49-----
tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

[M R P S I Q F L G L L L F W L H G
LEADER

103 tgctcagtgtgacatccagatgacacagtctccatcctçactgtctgcacatctct
103-----
acgagtcacactgttaggtctactgtgtcagaggttaggagtgacagacgttagaga

A Q C] [D I Q M T Q S P S S L S A S L
FR1

157 gggaggcaaagt caccatcacttgc aagacaagccaagacattaacaagtataat
157-----
ccctccgtttcagtggtagtgaacgttctgttcggttctgttaattgttcatata

G G K V T I T C] [K T S Q D I N K Y M
CDR1

211 ggcttggtaccaacacaaggcctggaaaacgtcctaggctgctcatacattacac
211-----
ccgaaccatggtgtgttggacctttgcaggatccgacgagtatgtaatgtg

A] [W Y Q H K P G K R P R L L I H] [Y T
FR2

265 atctgcattacagccaggcatccatcaagggttcagtggaaagtgggtctgggag
265-----
tagacgtaatgtcggtccgttagggtagttccaagtcacccitcaccagaccctc

S A L Q P] [G I P S R F S G S G S G R
CDR2

FIG. 11 A

319 agattattccttcaacatcagcaacccggagcctgaagatattgcaacttatta

tctaataaggaagtgttagtcgttggacctcgacttataaacgttgaataat

D Y S F N I S N L E P E D I A T Y Y
FR3

373 ttgtctacagtatgataatctgtggacgttcggtgaggcaccaagctggaaat

aacagatgtcatactattagacacacctgcaagccacccgtggtcgaccttta

C] [L Q Y D N L W T] [F G G G T K L E I
CDR3 FR4

427 caaacgggctgatgctgcaccaactgttatccatcttcccaccatccacccggaa

gtttgcccgactacgacgtggttgacataggtagaagggtggtaggtggccct

K]

AGG-5'

tcc

481 ---

agg

FIG. 11B

1 atgaaatgcagctgggtcatgttcttcgtatggcagtggttacaggg

1 tactttacgtcgaccaggatacaagaaggactaccgtcaccaatgtccc

[M K C S W V M F F L M A V V T G
LEADER .

49 gtcaattcagaggttcagctgcagcagtctggggcagagcttgtgaagccaggg

cagttaagtctccaagtgcacgtcgtcagacccgtctcgaacacttcggtccc
V N S}{E V Q L Q Q S G A E L V K P G
FR1

103 gcctcagtcaagttgtcctgcacagcttctggcttcaacattaaagacacatcat

cggagtcagttcaacaggacgtgtcgaagaccgaagttgttaatttctgtggata

A S V K L S C T A S G F N I K]{D T Y
CDR1

157 atacactgtgtgaagcagaggcctgaacagggcctggagtggattggaaggatt

tatgtgacacacttcgtctccggacttgcgtccggacacctcacctaacccttctaa
I H]{C V K Q R P E Q G L E W I G]{R I
FR2

211 gatcctgcgaatggttataactaaatatgacccgaagttccaggcaaggccact

ctaggacgcttaccaatatgatttatactggcttcaaggtcccggtccgggtga

D P A N G Y T K Y D P K F Q G]{K A T
CDR2

265 ataacagctgacacatcctccaacacacagcctacctgcagctcagcagcctgaca

tattgtcgactgtgttaggagggtgtcggatggacgtcgagtcgtcgactgt
I T A D T S S N T A Y L Q L S S L T
FR3

FIG. 12A

tctgaggacactgccgtctatttctgtgctagagagggatattatggtaactac
319 -----
agactcctgtgacggcagataaaagacacgatctccctataataccattgatg
S E D T A V Y F C A R] [E G Y Y G N Y
CDR3.

ggggtcatacgatggactactggggcaaggaacctcagtcaccgtctcctca
373 -----
ccccagatacgtacacctgtatgaccccagttccttggagtcagtggcagaggagt
G V Y A M D Y] [W G Q C T S V T V S . S]

gccaaaacgacaccccatctgtctatccactggcccgggatcc
427 -----
cggttttgctgtggggtagacagataggtgaccgggcctagg
S . S]

FIG. 12B

	FR1	CDR1	FR2	CDR2
	1	2	3	4
	12345678901234567890123	45678901234	567890123456789	0123456
	*	*****	*	***
21.6	DIQMTQSPSSLSASLGGKVITC	KTSQDINKYMA	WYQHKGKPRPLLH	YTSALQP
REI	DIQMTQSPSSLSASVGDRVITC	QASQDIKYLN	WYQQTPGKAPKLLIY	EASNLQA
La	DIQMTQSPSSLSASVGDRVITC	KTSQDINKYMA	WYQQTPGKAP <u>R</u> LLH	YTSALQP
Lb	-----	-----	R-----	-----

	FR3	CDR3	FR4		
	6	7	8	9	10
	78901234567890123456789012345678	901234567	8901234567	*****	
21.6	GIPSREFSGSGSGRDYSFNISNLEPEDIATYYC	LQYDNL-WT	FGGGTKLEIK		
REI	GVPSRFSGSGSGTDYTFTISSLQPEDIA TYYC	QQYQSLPYT	FGQGTKLQIT		
La	GIPSREFSGSGSG <u>R</u> DYTFTISSLQPEDIA TYYC	LQYDNL-WT	FGQGTK <u>V</u> EIK		
Lb	-I-----R-----	-----	-----	VE-K	

b
FIG. 13

FR1	CDR1	FR2	CDR2		
1	2	3	4	5	6
123456789012345678901234567890	12345	67890123456789	012A3456789012345		
*****			*****		

21.6 EVQLQQSGAELVKPGASVKSCTASGFNIK DTYIH CVKQRPEQGLEWIG RIDPANGYTKYDPKFQG

2*CL QVQLVQSGAEVKPGASVKSCKASGYTFT SYAMH WVRQAPGQRLEWMG WINAGNGNTKYSQKFQG

Ha QVQLVQSGAEVKPGASVKSCKASGFNIK DTYIH WVRQAPGQRLEWMB RIDPANGYTKYDPKFQG

Hb -----FNIK-----G-----

Hc -----FNIK-----

FR3	CDR3	FR4		
7	8	9	10	11
67890123456789012ABC345678901234	567890ABCDEF12	34567890123		
*	*			

21.6 KATITADTSSNTAYLQLSSLTSEDTAVYFCAR EGYYGNYGVYAMDY WGQGTSVTVSS

2*CL RVTITRDTSASTAYMELSSLRSEDTAVYYCAR GGYYGSGS---NY WGQGTLVTVSS

Ha RVTITADTSASTAYMELSSLRSEDTAVYYCAR EGYYGNYGVYAMDY WGQGTLVTVSS

Hb -----A-----

Hc -----A-----F-----

FIG. 14

HindIII KOZAK SEQUENCE

1 aagcttgcacccaccatgagaccgtctattcagttcctggggctcttgttgttc

ttcgaacggcggtggtaactctggcagataagtcaaggaccccgagaacaacaag

[M R P S I Q F L G L L L F
LEADER

55 tggcttcatggtgctcagtgtgacatccagatgacacagtctccatcctcactg

accgaagtaccacgagtcacactgttaggtctactgtgtcagaggtaggagtgac

W L H G A Q C] [D I Q M T Q S P S S L
FR1

109 tctgcattGTAggaGATAGAgtcaccatcacttgcagacaagccaagacatt

agacgtagaCATcctCTATCTcagtggtagtgaacgttctgttgcgttctgtaa

S A S V G D R V T I T C] [K T S Q D I
CDR1

163 aacaagtataatggcttggtagccaaCAGACAcctggaaaaGCTcctaggctgctc

ttgttcatataccgaaccatggtagtCTGTggacctttCGAggatccgacgag

N K Y M A] [W Y Q Q T P G K A P R L L
FR2

217 atacattacacatctgcattacagccaggcatcccataaggtagtggaaagt

tatgtaatgttagacgtaatgtcggtccgtaggtagttccaaagtcacattca

I H] [Y T S A L Q P] [G I P S R F S G S
CDR2

271 gggctgggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt

cccagaccctctctaataTGAAagTGGtagtcgTCGgacGTCggacttctataaa

G S F R D Y T F T I S S L Q P E D I
FR3

FIG. 15A

325 gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc

cgttgaataataacagatgtcatactattagacacacctgcaagccaGTTccgtgg

A T Y Y C] [L Q Y D N L W T] [F G Q G T
CDR3 FR4

379 SPLICE DONOR SITE BamHI
aagGTGgaaatcaaacgtgagtggatcc

ttcCACcttagttgcactcacctagg

K V E I K}

FIG. 15B

HindIII KOZAK SEQUENCEAAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTTTTGCCCTGCTGCCGTG1 -----
TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC[M D W T W R V F C L L A V
LEADER55 -----
GCTCCTGGGGCCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
CGAGGACCCCCGGTGTGGTCCACGTTGATCACGTCAAGGCCGCGGCTTCACTTC

A P G A H S] { Q V Q L V Q S G A E V K,

109 -----
AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacataaa
TTTGGGCCACGAAGGCACTTTCAGTCGACATTGATGCCAaagtgtatatttK P G A S V K V S C K A S G F N I K] {
FR1163 -----
gacacctatacacactGGGTTAGACAGGCCCTGGCCAAggCTgGAGTGGATg
ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTACD T Y I H] { W V R Q A P G Q R L E W M
CDR1 FR2

FIG. 16A

217 GGaaggattgatccgcgaatggttataactaaatatgacccgaagttccagggc

CCttcttaacttaggacgttaccaatatgatttatactgggcttcaaggccccg

G][R I D P A N G Y T K Y D P K F Q G][
CDR2

271 cgggtcACCatcACCgcgaGACACCTCTgccagcACCGCCTACATGGAACGTGTC

gcccagTGGtagTGGcgCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG

R V T I T A D T S A S T A Y M E L S
FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat

TCGGACGCGAGGCTCTGTGACGTCAGATGATGACGCCGtctccctataata

S L R S E D T A V Y Y C A R][E G Y Y

379 ggttaactacgggtctatgctatgACTAcTGGGGtCAaGGaACCCTTGTCAAC

ccattgatccccagatacgtacCTGATgACCCCaGTtCCtTGGAACAGTGG

G N Y G V Y A M D Y][W G Q G T L V T
CDR3
FR4

433 SPLICE DONOR SITE BamHI
GTCTccTCAGGTGAGTGGATCC

CAGaggAGTCCACTCACCTAGG

V S S]

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
Ile Lys - C

FIG. 17B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
Ala Arg Gly Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Cys Tyr Arg Gly Asp
Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C

FIG. 18B